



#3

1

SEQUENCE LISTING

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<120> THERMAL TOLERANT MANNANASE FROM ACIDOTHERMUS
CELLULOLYTICUS

<130> 40197.7US01

<140> 09/917,378
<141> 2001-07-28

<160> 8

<170> PatentIn Ver. 2.1

<210> 1
<211> 762
<212> PRT
<213> Acidothermus cellulolyticus

<400> 1
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35 40 45
Phe Val Leu Asn Gly Leu Pro Tyr Arg Tyr Gly Gly Thr Asn Asn Tyr
50 55 60
Tyr Leu Ser Tyr Gln Ser His Ala Asp Val Asp Asp Val Leu Ala Lys
65 70 75 80
Ala Gln Ala Met Asn Leu Ser Val Ile Arg Thr Trp Gly Phe Ile Asp
85 90 95
Ile Gly Ser Leu Asp Gly Ser Val Pro Thr Ile Asp Gly Asn Lys Asn
100 105 110
Gly Phe Tyr Phe Gln Tyr Trp Asp Pro Ser Thr Gly Ala Pro Ala Tyr
115 120 125
Asn Asp Gly Pro Thr Gly Leu Gln Gly Leu Asp Tyr Ala Ile Ala Ser
130 135 140
Ala Ala Ala His Gly Leu Arg Val Ile Val Val Leu Thr Asn Asp Trp
145 150 155 160
Lys Glu Phe Gly Gly Met Asp Gln Tyr Asp Lys Trp Tyr Gly Leu Pro
165 170 175

Tyr	His	Asp	Asn	Phe	Tyr	Thr	Asp	Pro	Arg	Thr	Gln	Gln	Ala	Tyr	Lys	180	185	190	
Asn	Trp	Val	Asn	His	Leu	Leu	Asn	Arg	Val	Asn	Ser	Ile	Thr	Gly	Val	195	200	205	
Thr	Tyr	Lys	Asn	Asp	Pro	Thr	Ile	Phe	Ala	Trp	Glu	Leu	Ala	Asn	Glu	210	215	220	
Pro	Arg	Cys	Val	Gly	Ser	Gly	Thr	Leu	Pro	Thr	Ser	Gly	Thr	Cys	Thr	225	230	235	240
Gln	Ala	Thr	Ile	Val	Asn	Trp	Val	Asp	Gln	Met	Ser	Ala	Tyr	Val	Lys	245	250	255	
Ser	Ile	Asp	Pro	Asn	His	Met	Val	Ser	Val	Gly	Asp	Glu	Gly	Phe	Tyr	260	265	270	
Ile	Gly	Ser	Thr	Gln	Gly	Ser	Gly	Trp	Pro	Tyr	Asn	Asp	Pro	Ser	Asp	275	280	285	
Gly	Val	Asp	Asn	Asn	Ala	Leu	Leu	Arg	Val	Lys	Asn	Ile	Asp	Phe	Gly	290	295	300	
Thr	Tyr	His	Leu	Tyr	Pro	Asn	Tyr	Trp	Gly	Gln	Asn	Ala	Asp	Trp	Gly	305	310	315	320
Thr	Gln	Trp	Ile	Lys	Asp	His	Ile	Ala	Asn	Ala	Ala	Ala	Ile	Gly	Lys	325	330	335	
Pro	Thr	Ile	Leu	Glu	Glu	Phe	Gly	Trp	Gln	Thr	Pro	Asp	Arg	Asp	Ser	340	345	350	
Val	Tyr	Gln	Thr	Trp	Thr	Gln	Thr	Val	Arg	Thr	Asn	Gly	Glu	Ala	Gly	355	360	365	
Trp	Asn	Phe	Trp	Met	Leu	Ala	Gly	Asn	Val	Asn	Gly	Gln	Pro	Tyr	Pro	370	375	380	
Asn	Tyr	Asp	Gly	Phe	Asn	Val	Tyr	Tyr	Pro	Ser	Ser	Thr	Ala	Thr	Val	385	390	395	400
Leu	Ala	Ser	Glu	Ala	Leu	Ala	Ile	Ser	Thr	Gly	Thr	Ser	Pro	Pro	Pro	405	410	415	
Ser	Pro	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Pro	Ser	Pro	Ser	Pro	Ser	Pro	420	425	430	
Ser	Ala	Ser	Pro	Ser	Ala	Ser	Pro	Ser	Ala	Ser	Ser	Ser	Pro	Ser	Pro	435	440	445	
Ser	Pro	Ser	Ser	Ser	Pro	Val	Ser	Gly	Gly	Val	Lys	Val	Gln	Tyr	Lys	450	455	460	
Asn	Asn	Asp	Ser	Ala	Pro	Gly	Asp	Asn	Gln	Ile	Lys	Pro	Gly	Leu	Gln	465	470	475	480

Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr Val
 485 490 495
 Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn
 500 505 510
 Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly
 515 520 525
 Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser
 530 535 540
 Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln
 545 550 555 560
 Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Asp Glu Thr Asn Asp
 565 570 575
 Tyr Ser Tyr Gly Thr Asn Thr Ala Phe Gln Asp Trp Thr Lys Val Thr
 580 585 590
 Val Tyr Val Asn Gly Arg Leu Val Trp Gly Thr Glu Pro Ser Gly Thr
 595 600 605
 Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro
 610 615 620
 Ser Pro Thr Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro
 625 630 635 640
 Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro
 645 650 655
 Ser Val Ser Ser Ser Gly Val Gly Cys Arg Ala Thr Tyr Val Val Asn
 660 665 670
 Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr
 675 680 685
 Gly Ser Arg Ala Thr Ser Gly Trp Thr Val Ala Trp Ser Phe Gly Gly
 690 695 700
 Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly
 705 710 715 720
 Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile Gln Pro
 725 730 735
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 740 745 750
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<210> 2

<211> 2289

<212> DNA

<213> Acidothermus cellulolyticus

<400> 2

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<210> 3

<211> 375

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GH5 catalytic domain

<400> 3

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Ala Pro Ala Gly Phe Val Thr Ala Ser Gly Gly Gln Phe Val Leu Asn
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Gly	Leu	Pro	Tyr	Arg	Tyr	Gly	Gly	Thr	Asn	Asn	Tyr	Tyr	Leu	Ser	Tyr			
			20					25					30					
Gln	Ser	His	Ala	Asp	Val	Asp	Asp	Val	Leu	Ala	Lys	Ala	Gln	Ala	Met			
		35					40					45						
Asn	Leu	Ser	Val	Ile	Arg	Thr	Trp	Gly	Phe	Ile	Asp	Ile	Gly	Ser	Leu			
	50					55					60							
Asp	Gly	Ser	Val	Pro	Thr	Ile	Asp	Gly	Asn	Lys	Asn	Gly	Phe	Tyr	Phe			
65					70					75					80			
Gln	Tyr	Trp	Asp	Pro	Ser	Thr	Gly	Ala	Pro	Ala	Tyr	Asn	Asp	Gly	Pro			
				85					90						95			
Thr	Gly	Leu	Gln	Gly	Leu	Asp	Tyr	Ala	Ile	Ala	Ser	Ala	Ala	Ala	His			
			100					105						110				
Gly	Leu	Arg	Val	Ile	Val	Val	Leu	Thr	Asn	Asp	Trp	Lys	Glu	Phe	Gly			
		115					120					125						
Gly	Met	Asp	Gln	Tyr	Asp	Lys	Trp	Tyr	Gly	Leu	Pro	Tyr	His	Asp	Asn			
	130					135					140							
Phe	Tyr	Thr	Asp	Pro	Arg	Thr	Gln	Gln	Ala	Tyr	Lys	Asn	Trp	Val	Asn			
145					150					155					160			
His	Leu	Leu	Asn	Arg	Val	Asn	Ser	Ile	Thr	Gly	Val	Thr	Tyr	Lys	Asn			
				165				170						175				
Asp	Pro	Thr	Ile	Phe	Ala	Trp	Glu	Leu	Ala	Asn	Glu	Pro	Arg	Cys	Val			
			180					185					190					
Gly	Ser	Gly	Thr	Leu	Pro	Thr	Ser	Gly	Thr	Cys	Thr	Gln	Ala	Thr	Ile			
		195					200					205						
Val	Asn	Trp	Val	Asp	Gln	Met	Ser	Ala	Tyr	Val	Lys	Ser	Ile	Asp	Pro			
	210					215					220							
Asn	His	Met	Val	Ser	Val	Gly	Asp	Glu	Gly	Phe	Tyr	Ile	Gly	Ser	Thr			
225					230					235					240			
Gln	Gly	Ser	Gly	Trp	Pro	Tyr	Asn	Asp	Pro	Ser	Asp	Gly	Val	Asp	Asn			
				245				250						255				
Asn	Ala	Leu	Leu	Arg	Val	Lys	Asn	Ile	Asp	Phe	Gly	Thr	Tyr	His	Leu			
			260				265						270					
Tyr	Pro	Asn	Tyr	Trp	Gly	Gln	Asn	Ala	Asp	Trp	Gly	Thr	Gln	Trp	Ile			
		275					280						285					
Lys	Asp	His	Ile	Ala	Asn	Ala	Ala	Ala	Ile	Gly	Lys	Pro	Thr	Ile	Leu			
	290					295					300							
Glu	Glu	Phe	Gly	Trp	Gln	Thr	Pro	Asp	Arg	Asp	Ser	Val	Tyr	Gln	Thr			
305					310					315					320			

Trp	Thr	Gln	Thr	Val	Arg	Thr	Asn	Gly	Glu	Ala	Gly	Trp	Asn	Phe	Trp
				325					330					335	
Met	Leu	Ala	Gly	Asn	Val	Asn	Gly	Gln	Pro	Tyr	Pro	Asn	Tyr	Asp	Gly
			340					345					350		
Phe	Asn	Val	Tyr	Tyr	Pro	Ser	Ser	Thr	Ala	Thr	Val	Leu	Ala	Ser	Glu
		355					360					365			
Ala	Leu	Ala	Ile	Ser	Thr	Gly									
	370					375									

```
<210> 4
<211> 154
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Carbohydrate binding domain

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<400> 4
Val Ser Gly Gly Val Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro
  1          5          10          15

Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser
          20          25          30

Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
          35          40          45

Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
  50          55          60

Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
  65          70          75          80

Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu
          85          90          95

Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser
          100          105          110

Asp Trp Ser Asn Phe Asp Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn
          115          120          125

Thr Ala Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Arg
          130          135          140

Leu Val Trp Gly Thr Glu Pro Ser Gly Thr
          145          150

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```
<210> 5
<211> 101
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Carbohydrate binding domain

<400> 5

Gly Val Gly Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser
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Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr
 20 25 30

Ser Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr
 35 40 45

Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala
 50 55 60

Thr Asn Leu Ser Tyr Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr
 65 70 75 80

Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Thr Ala Pro Thr Leu
 85 90 95

Thr Cys Thr Ala Ser
 100

<210> 6

<211> 375

<212> PRT

<213> Acidothermus cellulolyticus

<400> 6

Ala Pro Ala Gly Phe Val Thr Ala Ser Gly Gly Gln Phe Val Leu Asn
 1 5 10 15

Gly Leu Pro Tyr Arg Tyr Gly Gly Thr Asn Asn Tyr Tyr Leu Ser Tyr
 20 25 30

Gln Ser His Ala Asp Val Asp Asp Val Leu Ala Lys Ala Gln Ala Met
 35 40 45

Asn Leu Ser Val Ile Arg Thr Trp Gly Phe Ile Asp Ile Gly Ser Leu
 50 55 60

Asp Gly Ser Val Pro Thr Ile Asp Gly Asn Lys Asn Gly Phe Tyr Phe
 65 70 75 80

Gln Tyr Trp Asp Pro Ser Thr Gly Ala Pro Ala Tyr Asn Asp Gly Pro
 85 90 95

Thr Gly Leu Gln Gly Leu Asp Tyr Ala Ile Ala Ser Ala Ala Ala His
 100 105 110

Gly Leu Arg Val Ile Val Val Leu Thr Asn Asp Trp Lys Glu Phe Gly
 115 120 125

Gly Met Asp Gln Tyr Asp Lys Trp Tyr Gly Leu Pro Tyr His Asp Asn
 130 135 140
 Phe Tyr Thr Asp Pro Arg Thr Gln Gln Ala Tyr Lys Asn Trp Val Asn
 145 150 155 160
 His Leu Leu Asn Arg Val Asn Ser Ile Thr Gly Val Thr Tyr Lys Asn
 165 170 175
 Asp Pro Thr Ile Phe Ala Trp Glu Leu Ala Asn Glu Pro Arg Cys Val
 180 185 190
 Gly Ser Gly Thr Leu Pro Thr Ser Gly Thr Cys Thr Gln Ala Thr Ile
 195 200 205
 Val Asn Trp Val Asp Gln Met Ser Ala Tyr Val Lys Ser Ile Asp Pro
 210 215 220
 Asn His Met Val Ser Val Gly Asp Glu Gly Phe Tyr Ile Gly Ser Thr
 225 230 235 240
 Gln Gly Ser Gly Trp Pro Tyr Asn Asp Pro Ser Asp Gly Val Asp Asn
 245 250 255
 Asn Ala Leu Leu Arg Val Lys Asn Ile Asp Phe Gly Thr Tyr His Leu
 260 265 270
 Tyr Pro Asn Tyr Trp Gly Gln Asn Ala Asp Trp Gly Thr Gln Trp Ile
 275 280 285
 Lys Asp His Ile Ala Asn Ala Ala Ala Ile Gly Lys Pro Thr Ile Leu
 290 295 300
 Glu Glu Phe Gly Trp Gln Thr Pro Asp Arg Asp Ser Val Tyr Gln Thr
 305 310 315 320
 Trp Thr Gln Thr Val Arg Thr Asn Gly Glu Ala Gly Trp Asn Phe Trp
 325 330 335
 Met Leu Ala Gly Asn Val Asn Gly Gln Pro Tyr Pro Asn Tyr Asp Gly
 340 345 350
 Phe Asn Val Tyr Tyr Pro Ser Ser Thr Ala Thr Val Leu Ala Ser Glu
 355 360 365
 Ala Leu Ala Ile Ser Thr Gly
 370 375

<210> 7
 <211> 356
 <212> PRT
 <213> Agaricus bisporus

<400> 7
 Val Ser Thr Gly Phe Val Lys Ala Ser Gly Thr Arg Phe Thr Leu Asn
 1 5 10 15

Gly	Gln	Lys	Tyr	Thr	Val	Val	Gly	Gly	Asn	Ser	Tyr	Trp	Val	Gly	Leu	20	25	30	
Thr	Gly	Leu	Ser	Thr	Ser	Ala	Met	Asn	Gln	Ala	Phe	Ser	Asp	Ile	Ala	35	40	45	
Asn	Ala	Gly	Gly	Thr	Thr	Val	Arg	Thr	Trp	Gly	Phe	Asn	Glu	Val	Thr	50	55	60	
Ser	Pro	Asn	Gly	Asn	Tyr	Tyr	Gln	Ser	Trp	Ser	Gly	Ala	Arg	Pro	Thr	65	70	75	80
Ile	Asn	Thr	Gly	Ala	Ser	Gly	Leu	Leu	Asn	Phe	Asp	Asn	Val	Ile	Ala	85	90	95	
Ala	Ala	Lys	Ala	Asn	Gly	Ile	Arg	Leu	Ile	Val	Ala	Leu	Thr	Asn	Asn	100	105	110	
Trp	Ala	Asp	Tyr	Gly	Gly	Met	Asp	Val	Tyr	Val	Asn	Gln	Met	Val	Gly	115	120	125	
Asn	Gly	Gln	Pro	His	Asp	Leu	Phe	Tyr	Thr	Asn	Thr	Ala	Ile	Lys	Asp	130	135	140	
Ala	Phe	Lys	Ser	Tyr	Val	Arg	Thr	Phe	Val	Ser	Arg	Tyr	Ala	Asn	Glu	145	150	155	160
Pro	Thr	Val	Met	Ala	Trp	Glu	Leu	Ala	Asn	Glu	Pro	Arg	Cys	Lys	Gly	165	170	175	
Ser	Thr	Gly	Thr	Thr	Ser	Gly	Thr	Cys	Thr	Thr	Thr	Thr	Val	Thr	Asn	180	185	190	
Trp	Ala	Lys	Glu	Met	Ser	Ala	Phe	Ile	Lys	Thr	Ile	Asp	Ser	Asn	His	195	200	205	
Leu	Val	Ala	Ile	Gly	Asp	Glu	Gly	Phe	Tyr	Asn	Gln	Pro	Gly	Ala	Pro	210	215	220	
Thr	Tyr	Pro	Tyr	Gln	Gly	Ser	Glu	Gly	Val	Asp	Phe	Glu	Ala	Asn	Leu	225	230	235	240
Ala	Ile	Ser	Ser	Val	Asp	Phe	Ala	Thr	Phe	His	Ser	Tyr	Pro	Glu	Pro	245	250	255	
Trp	Gly	Gln	Gly	Ala	Asp	Ala	Lys	Ala	Trp	Gly	Thr	Gln	Trp	Ile	Thr	260	265	270	
Asp	His	Ala	Ala	Ser	Met	Lys	Arg	Val	Asn	Lys	Pro	Val	Ile	Leu	Glu	275	280	285	
Glu	Phe	Gly	Val	Thr	Thr	Asn	Gln	Pro	Asp	Thr	Tyr	Ala	Glu	Trp	Phe	290	295	300	
Asn	Glu	Val	Glu	Ser	Ser	Gly	Leu	Thr	Gly	Asp	Leu	Ile	Trp	Gln	Ala	305	310	315	320

Gly Ser His Leu Ser Thr Gly Asp Thr His Asn Asp Gly Tyr Ala Val
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Tyr Pro Asp Gly Pro Val Tyr Pro Leu Met Lys Ser His Ala Ser Ala
 340 345 350

Met Lys Asn Arg
 355

<210> 8

<211> 346

<212> PRT

<213> Trichoderma reesei

<400> 8

Arg Ala Ser Ser Phe Val Thr Ile Ser Gly Thr Gln Phe Asn Ile Asp
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Gly Lys Val Gly Tyr Phe Ala Gly Thr Asn Cys Tyr Trp Cys Ser Phe
 20 25 30

Leu Thr Asn His Ala Asp Val Asp Ser Thr Phe Ser His Ile Ser Ser
 35 40 45

Ser Gly Leu Lys Val Val Arg Val Trp Gly Phe Asn Asp Val Asn Thr
 50 55 60

Gln Pro Ser Pro Gly Gln Ile Trp Phe Gln Lys Leu Ser Ala Thr Gly
 65 70 75 80

Ser Thr Ile Asn Thr Gly Ala Asp Gly Leu Gln Thr Leu Asp Tyr Val
 85 90 95

Val Gln Ser Ala Glu Gln His Asn Leu Lys Leu Ile Ile Pro Phe Val
 100 105 110

Asn Asn Trp Ser Asp Tyr Gly Gly Ile Asn Ala Tyr Val Asn Ala Phe
 115 120 125

Gly Gly Asn Ala Thr Thr Trp Tyr Thr Asn Thr Ala Ala Gln Thr Gln
 130 135 140

Tyr Arg Lys Tyr Val Gln Ala Val Val Ser Arg Tyr Ala Asn Ser Thr
 145 150 155 160

Ala Ile Phe Ala Trp Glu Leu Gly Asn Glu Pro Arg Cys Asn Gly Cys
 165 170 175

Ser Thr Asp Val Ile Val Gln Trp Ala Thr Ser Val Ser Gln Tyr Val
 180 185 190

Lys Ser Leu Asp Ser Asn His Leu Val Thr Leu Gly Asp Glu Gly Leu
 195 200 205

Gly Leu Ser Thr Gly Asp Gly Ala Tyr Pro Tyr Thr Tyr Gly Glu Gly
 210 215 220

Thr	Asp	Phe	Ala	Lys	Asn	Val	Gln	Ile	Lys	Ser	Leu	Asp	Phe	Gly	Thr
225					230					235					240
Phe	His	Leu	Tyr	Pro	Asp	Ser	Trp	Gly	Thr	Asn	Tyr	Thr	Trp	Gly	Asn
				245					250					255	
Gly	Trp	Ile	Gln	Thr	His	Ala	Ala	Ala	Cys	Leu	Ala	Ala	Gly	Lys	Pro
			260					265					270		
Cys	Val	Phe	Glu	Glu	Tyr	Gly	Ala	Gln	Gln	Asn	Pro	Cys	Thr	Asn	Glu
		275					280					285			
Ala	Pro	Trp	Gln	Thr	Thr	Ser	Leu	Thr	Thr	Arg	Gly	Met	Gly	Gly	Asp
	290					295					300				
Met	Phe	Trp	Gln	Trp	Gly	Asp	Thr	Phe	Ala	Asn	Gly	Ala	Gln	Ser	Asn
305					310					315					320
Ser	Asp	Pro	Tyr	Thr	Val	Trp	Tyr	Asn	Ser	Ser	Asn	Trp	Gln	Cys	Leu
				325					330					335	
Val	Lys	Asn	His	Val	Asp	Ala	Ile	Asn	Gly						
			340					345							